

TELEPHONE: 317-276-3334
 TELEFAX: 317-276-3861
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1353 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: 1..1353

US-08-843-309-1

Alignment Scores:
 pred. No.: 1.87e-55
 score: 586.50
 Percent Similarity: 52.92%
 Best Local Similarity: 34.99%
 Query Match: 25.95%
 DB: 2

US-09-701-229-2 (1-448) x US-08-843-309-1 (1-1353)

QY **App.** 7 AspHisPheAspGlyLeuValGlyLeuGlyLeuGlySerGlyMetSerLeu 22
Surfat 13 GATCACTTAATAGAAGATGCTGTTAGTTGGCAAGCTGGAACTCTGCA 72

QY 23 ValArgTyrlLeuAlaLargArgGlyLeuProPheAlaValValAspThrArg 39
 ||||| ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 73 GCTCGTTGTTGACAGCTGGTGCATTTGACAGTAATGAACTGGAACTTCGAG 132
 QY 40 GluAsnProProGluLeuAlaThrLeuArgGlyAlaGlyTyrProGlnValGluValArgCys 59
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 133 GACAATCCAGTGCCCAAAGTTGCTGGAA-----GAGGGATCAGGTCTTACA 183
 QY 60 GlyGlu-----LeuAspAlaLysPheLeuAspGlyLeuGlyAspGlyAlaAsp 74
 ||||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 184 GGTGCCATCCTTGGAACTCTGGATGAAAGGTTGGCTTATGGTGAAG 234
 QY 75 ValSerProGlyLeuSerLeuArgThrProLysAlaLeuValGlnAlaAlaAlaLysLysVal 94
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 235 --AATCCAGTATCCCTACACATCCCTGATGAAAGGCTTTGGCCAGAGAATT 291
 QY 95 ArgLeuSerGlyAspIleAspPheAlaLysPheAlaLysAlaProIleValAlaLeu 114
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 292 CCAGTCCTGACTGGGGATTGGCTTATTTGATTCAGAGAACCGATTATGGTAC 351
 QY 115 ThrGlySerAlaAlaLysSerThrValThrLeuValGlyGluMetAlaValAla 134
 ||||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 352 ACAGGATCGAACGGTAAAGACACACACGACTATGGGAATTGGGGAGTTGGCTGCT 411
 QY 135 AspLysArgValAlaValGlyLysLeuGlyLysProLysAlaAspIleAspLeu 152
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 412 GGGCAGCATGGCTGTTTATGGGATATCGCTATCTGCGAGCTGGCTCAAATA 471
 QY 153 AlaAspAspIleGluLeuThrValLeuGluLeuSerSerPheGlnLeuGluThrCysAsp 172
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 472 GCATCAGATAGGGACAGCTGTTATGGAACCTTCTTCCTTCAACTCATGGGCTCA 531
 QY 173 ArgLeuAsnAlaLysAlaLysAlaLysAlaLysAlaLysAlaLysAlaLysAla 134
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 532 GAAATCCATCCAGAGATGGCTTATACCAACCTCATGCCACTCATGGGCTCA 591
 QY 193 AspGlyMetAlaAspIleGlyLysLeuLysIleAspIleAspLeuAlaAspThr 209
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 592 GGGTCATTTGAAATGAGCAGCAAGTGGAAATATCCGAAACAGTGACAGCAGCT 651
 QY 210 ArgGlyValValValAsnAlaGlyAlaAspAlaLeuThrArgProLeuIleAlaAspThr 228
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 652 GATTCTCTGCTGACTTTAATCAAGCTGGCAAAAGCTGACTTGCTCCAGACAGA 711

QY 229 -----ValProCysTrpSerPheGlyLeuAsnLysProAspIleLysAlaPheGly 245
 Db 712 GCCACTGTTGTCACATTTCAACAC-----CTTGAAAGTTGCT-----GGAA 753
 QY 246 LeuIleGluGluAspGlyGlyLysIlePheLeuAlaPheGlyIlePheAsnIleLeuProVal 265
 Db 754 GCTTATCTGGAGAGTGGTCA-----CTCTACTTGCGTGACTCTGACTCATGGCAGC 807
 QY 266 GlyGluIleLeuIleArgGlyIleAlaAspIleSerAlaAspAlaLeuLeuIleLeu 285
 Db 808 ATGAAACCGGTTGTCAGGTAGCCACAAATUTCGAAATGCCCTTGCGACTATGCTGA 867
 QY 286 GLYHISALAVAlGlyIleProPheAspAlaMetAlaLeuGlyAlaLeuIleAlaProSerGly 305
 Db 868 GCCANGCCTTCGTCATGCTGGACATCAACCATCAGAGAACTCTTCAGCCTCGGCT 927
 QY 306 LeuAlaHisArgCysGlnIlePheAlaArgGlyGlyValSerIleTyrAspSer 325
 Db 928 GTCACAAACACGCTCTGCTGAGTCAGCTGAGCTGAGCTAACATGCTATAACGAC 987
 QY 326 LysAlaThrAsnValGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAsp 345
 Db 988 AAATCACTAACTATCTGGCTACTCAAACGCTTTCAGGTTGAC-----AAC 1038
 QY 346 GlyLysLeuValLeuAlaIleGlyIleAspGlyIleGlyAlaAlaPheIleAspLeuArg 365
 Db 1039 AGCAAGGTGCGCTTGTGATGCGAGGTCGCTGACCTGCGCATGTTGCGAATG 1095
 QY 366 GluProValAlaArgPheCysArgAlaValValLeuLeuGlyIleAspAlaAspIleAsp 385
 Db 1096 GTGCCAGACATCTGGACTCAAGAGGCTTTCAGGTTGAC 1155
 QY 386 AlaGlnAlaIleGlyAsnAla-----ValProLeuValArgValAlaThrLeuAspGluAla 404
 Db 1156 AAACGGCGACGACAGGGCTGCTGCTGCTTGCGAGGCGACAGAATTGCGATGCC 1215
 QY 405 ValArgGlnAlaAlaIleGlyIleAlaIleGlyIleLeuLeuIleLeuSerProAlaCys 424
 ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| ||||| ::||| |||||
 Db 1216 ACCCGGAAGGCCATATGAGCTTGCGACTCAGGAGATGTTGCTCTCTGTCGCAAT 1275
 QY 425 AlaSerLeuAspPheIleGlyAsnIleGlyIleGluGlyIleGlyArgLeuIleAlaLysAla 444
 Db 1276 GCGAGCTGGGATATGCTGCTACGTTGAGTCGTTGAGTCGTTGGGGACCTTATCGCACACTTA 1335
 QY 445 GluGluIle 447
 Db 1336 GCGGAGTTA 1344

Search completed: August 14, 2003, 09:37:52
 Job time : 1636 secs

Sequence of
 US Pat. 5,834,270
 MurD protein

SEQ ID 2

ALIGNMENTS

RESULT 1
US-09-252-991A-7702
; Sequence 7702, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7702
LENGTH: 1371
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7702

Alignment Scores:

Pred. No.:	0	Length:	1371
Score:	448.00	Matches:	448
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-701-229-2 (1-448) x US-09-252-991A-7702 (1-1371)

Qy	1 MetSerLeuIleAlaSerAspHisPheArgIleValValGlyLeuGlyLysSerGlyMet 20
Db	25 ATGAGCCTGATCGCCTCCGACCCTTCCGCATCGTTGTCGGCCTCGGCAAGAGCGGCATG 84

Applicant
Is speed
patent

Db 978 AGCACCGTGACCACTTGGTGGCCAAATGGGGTGCGCGGACAGCGTGCAGCGC 919
 Qy 141 GLYCLysAlaSerLeuGlyLysLeuProAlaLeuAspLeuAlaAspAspIleLeuLeuTyrVal 160
 Db 918 GCGGCCAACCTGGCACCCGGCGCAGACATGGCGACATGGCTGAGCTGACCTGACCTG 859
 Qy 161 LeuGluLeuSerSerDipeGlnLeuGluLysCysAspArgLeuAsnAlaGluValLeuThr 180
 Db 858 TTGAGCTGTCGAGCTCCAGCTGGAACTGGATGCCAACGGCGAGGTTGGAC 799
 Qy 181 ValLeuAlaValSerIleAspIleAlaPhisMetAspArgTyrAspGlyMetAlaAspTyrIle 200
 Db 798 GIGCAGACGTCAGCCACATGGATGCTACGGCATGGCTGACTACCTG 739
 Qy 201 AlaLeuIleAspIleAspLeuGlyLysGlyAlaArgGlnValValAlaValAsnArgAlaAspAlaLeu 220
 Db 738 GCGAACGACCGGATCCTCCGGTGGCCGGCAGCTGCTG 679
 Qy 221 ThrArgProLeuAlaLeuGlyLeuProCysTyrSerPhedGlyLeuAsnLysProAsp 240
 Db 678 ACCGACGCCGATGCCGATACCGTACCGCTGGCTGCTGGCTGACAGCCGAC 619
 Qy 241 PhelAspAlaPhedGlyLeuIleGluGluAspGlyGlnLysTopleAlaPhedGlyLeuAsp 260
 Db 618 TTCAKCGCTTGGCTGATCGAGGAAGCGCCAGAGGCTGCTGGCTGAGCTG 559
 Qy 261 LysLeuLeuProValGlyGluLeuIleGlyLeuGlyLeuLeuAsnTyrSerAsnAlaLeu 280
 Db 558 AAGCTCTGGCGGTTGGCAACTGAGATCGATCGCTGGCCACAACTATTCAGCGCTC 499
 Qy 281 AlaAlaLeuLeuLeuGlyHisAlaValAlaGlyLeuProLeuProLeuAsnTyrSerAsnAlaLeu 300
 Db 498 GCGCCCTGGCGTGGCCATGGCTGGCTGGCTGGCTGGCTGGCCATGGCTGGCGCTG 439
 Qy 301 LysAlaPheSerGlyLeuAlaHisArgCysGlnTyrValArgGluArgGlyLysSer 320
 Db 438 AGGGCTTTCGGCCGCTCATCCTGCGAGTGGTACGGACGGCGAGGGCTGGAC 379
 Qy 321 TyrTyrAspAspSerLysAlaThrAsnValGlyAlaAlaLeuAlaAlaIleGlyLeu 340
 Db 378 TACTACGAGTCAGTCAGGCCACGGCCGCGCCCTGGGGGGATCGAGGGCTG 319
 Qy 341 GlyAlaAspIleAspGlyLysLeuValLeuAlaIleGlyGlyAspGlyLysGlyAlaAsp 360
 Db 318 GCTGCCACATCGAGCCGCAAGCTGGCTCTCGCCGGGAGACGGCAGGGCCGAT 259
 Qy 361 PheHisAspLeuArgTyrProValAlaArgPhedGlyCysArgAlaValAlaValLeuLeuGlyArg 380
 Db 258 TTCTTGACTGGGGAGCCGGTTCCTCCGGCGGGTGTACGCTGGCGCT 199
 Qy 381 AspAlaGlyLeuIleAlaGlnAlaLeuIleGlyAsnAlaValProLeuValArgValAlaThr 400
 Db 198 GACGCCGGCTGATGCCAGCACTGGCACCGGGTGGCTGGCGCAAG 139
 Qy 401 LeuAspGluAlaValArgGlnAlaAlaGluLeuAlaArgGluGlyAspAlaValLeuLeu 420
 Db 138 CTGGACGAGKAGCACTGGCGGAGGCCGAGCTGGCAAGCGGATGGCTGGT 79
 Qy 421 SerProAlaCysAlaSerIleAspMetPhedGlyAspGluIleArgGlyArgLeuIlePhe 440
 Db 78 TCGCCGCCGCGCAGCCCTGAGCTGGCCGGAGGAGGGCGAGGGCTGTC 19
 Qy 441 AlaValAlaValGluGlu 446
 Db 18 GCGAAACCCGTAGAGAG 1

RESULT 3
 US-09-252-991A-7787/c
 Sequence 7787, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ORGANISM: *Pseudomonas aeruginosa*
 SEQ ID NO: 7787
 LENGTH: 567
 TYPE: DNA
 ;
 US-09-252-991A-7787
 ;
 Alignment Scores:
 Pred. No.: 1.73e-175 Length: 567
 Score: 188.00 Matches: 188
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 41.96% Indexes: 0
 DB: 4 Gaps: 0

US-09-701-229-2 (1-448) x US-09-252-991A-7787 (1-567)

Qy 242 LysAlaPhedGlyLeuIleGluGluAspGlyGlnLysTopleAlaPhedGlnPhedAspLys 261
 Db 565 AAGCTTTCGGCTGATCGAGGAGACGGCCAGAGTCCTGGCTCCAGTCAGTCAG 506
 Qy 262 LeuLeuProValGlyGluLeuIleGlyLeuGlyAlaAlaAsnTyrSerAsnAlaLeu 281
 Db 505 CTGCTCCGGTTGGCACTGAGAATCCACGGCTGGCCACACTATTCACGCCCTGG 446
 Qy 282 AlaLeuAlaLeuGlyHisAlaValAlaGlyLeuProLeuAspAlaLeuLeuGlyLys 301
 Db 445 GCGCTGGGGCATGGTGGCCACCGGCTGAGCTGGCCATGGCTGGCGCTGG 386
 Qy 302 AlaPheSerGlyLeuIleGlyLeuIleGlyLeuGlyAlaAlaAsnTyrSerAsnAlaLeu 321
 Db 385 GCGCTGGGGCTGGCACTGAGAATCCACGGCTGGCCACACTATTCACGCCCTGG 326
 Qy 322 TyrAspAspSerLysAlaThrAsnValGlyAlaAlaLeuAlaLeuAlaLeuGlyLeu 341
 Db 325 TACGAGCATTCAGGCCACAGCTGGCTCTGGGGGGATCGAGGGCTGG 266
 Qy 342 AlaAspIleAspGlyLysLeuValLeuAlaIleGlyGlyAspGlyLysGlyAlaAsp 361
 Db 265 GCGCACATCCAGCGCAAGGGGGTGTCTGGCCGGAGCACGCAAGGGGGATGTC 206
 Qy 362 HisAspLeuArgGluProValAlaArgPheCysArgAlaValValLeuLeuGlyArgAsp 381
 Db 205 CATGACGATTCAGGCCACAGCTGGCTCTGGGGGGATCGAGGGCTGG 146
 Qy 382 AlaGlyLeuIleAlaGlnAlaLeuGlyAsnAlaValProLeuValArgValAlaThrIle 401
 Db 145 GCGCGCTGATGGCCAGCGCAGCTGGCAAGCGCTGAGCTGGCTGGCGCTGAC 86
 Qy 402 AspGluAlaValArgGlnAlaAlaGluLeuAlaArgGluGlyAspAlaValLeuLeu 421
 Db 85 GACGAGCACTCCACGGCCAGGGGGAGTGGCCGGAGGGCGAGGGCTGG 26
 Qy 422 ProIleCysAlaSerLeuAspMet 429
 Db 25 CGCGCTGGCGGACCTGGACATG 2

RESULT 4
 US-09-252-991A-7928/c
 Sequence 7928, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09-252, 991A
 PRIORITY FILING DATE: 1998-02-18
 PRIORITY APPLICATION NUMBER: US 60/094, 190
 PRIORITY FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 7787
 LENGTH: 567
 TYPE: DNA
 ;
 US-09-252-991A-7787
 ;
 Alignment Scores:
 Pred. No.: 1.73e-175 Length: 567
 Score: 188.00 Matches: 188
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 41.96% Indexes: 0
 DB: 4 Gaps: 0

SEQ ID 1

100

RESULT 1
US-09-252-991A-7861/c
; Sequence 7861, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7861
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7861

Query Match 81.6%; Score 1183; DB 4; Length 1401;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GTGCTGATCGGCCCTGCCACCTTGAAGCTGCGTTGAGGACGAAGAGAGCATGAGCCTGAT 61
Db 1387 GTGCTGATCGGCCCTGCCACCTTGAAGCTGCGTTGAGGACGAAGAGAGCATGAGCCTGAT 1328
Qy 62 CGCCTCCGACCACTCCGCATCGTTGTCGGCTCGGCAAGAGCGGCATGTCCTGGTGG 121
Db 1327 CGCCTCCGACCACTCCGCATCGTTGTCGGCTCGGCAAGAGCGGCATGTCCTGGTGG 1268
Qy 122 CTACCTGGCCGCCGGCTTGCCTTCGCCGTGGTCGATAACCGAGAGAACCCGCCGA 181
Db 1267 CTACCTGGCGGCCGGCTTGCCTTCGCCGTGGTCGATAACCGAGAGAACCCGCCGA 1208
Qy 182 GCTGGCCACCCCTGCGTGCCCCAGTATCCGCAGGTGGAAAGTGGCTGGCGAACCTCGACGC 241
Db 1207 GCTGGCCACCCCTGCGTGCCCCAGTATCCGCAGGTGGAAAGTGGCTGGCGAACCTCGACGC 1148
Qy 242 CGAGTTCCTCTGCTCCGCCCGCGAACCTACGTCAGCCCCGGCTTGCGCTGCCAACCCC 301
Db 1147 CGAGTTCCTCTGCTCCGCCCGCGAACCTACGTCAGCCCCGGCTTGCGCTGCCAACCCC 1088
Qy 302 TCGCTGGTACAGGCCGCCCGAAGGGCTGCGCATCTCCGGTGACATCGATCTTCGC 361
Db 1087 CGCGCTGGTACAGGCCGCCCGAAGGGCTGCGCATCTCCGGTGACATCGATCTTCGC 1028

QY 62 CGCCCTCCGACACTTCCGATCCCTGCGGCCAGAGCGGGCATGTCCTGGGG 121 ; Sequence 9277; Application US/09252991A
 Db 60 CGCTCCGACACTTCCGATCCCTGCGGCCAGAGCGGGCATGTCCTGGGG 1 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/074, 788
 ; PRIORITY DATE: 1998-02-18
 ; PRIORITY NUMBER: US 60/094, 190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 7860
 ; LENGTH: 1287
 ; TYPE: DNA
 ; ORGANISM: *Pseudomonas aeruginosa*
 ; US-09-252-991A-7600

Query Match 4.3%; Score 62; DB 4; Length 1287;
 Best Local Similarity 100.0%; Pred. No. 2.7e-19;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1389 CTAGCGTGTGCGCTGGTGTGCGCCCTTCCGTCGGCGCTGTGAGCCGGACGGCA 1448 ; Sequence 1743; Application US/09252991A
 Db 1287 CTAGCGTGTGCGCTGGTGTGCGCCCTTCCGTCGGCGCTGTGAGCCGGACGGCA 1228 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/074, 788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY NUMBER: US 60/094, 190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 1743
 ; LENGTH: 405
 ; TYPE: DNA
 ; ORGANISM: *Pseudomonas aeruginosa*
 ; US-09-252-991A-7623

RESULT 9
 US-09-252-991A-7623
 ; Sequence 7623; Application US/09252991A
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/094, 190
 ; PRIORITY FILING DATE: 1998-07-27
 ; PRIORITY NUMBER: US 60/094, 190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 1743
 ; LENGTH: 405
 ; TYPE: DNA
 ; ORGANISM: *Pseudomonas aeruginosa*
 ; US-09-252-991A-7623

Query Match 2.05%; Score 36; DB 4; Length 1404;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGCTGATCGGCCGACCTTGAAAGCTGGGTGA 37 ; Sequence 12452; Application US/09252991A
 Db 1369 GTGCTGATCGGCCGACCTTGAAAGCTGGGTGA 1404 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/074, 788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY NUMBER: US 60/094, 190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 1743
 ; LENGTH: 1404
 ; TYPE: DNA
 ; ORGANISM: *Pseudomonas aeruginosa*
 ; US-09-252-991A-7623

RESULT 12
 US-09-252-991A-12452/C
 ; Sequence 12452; Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/074, 788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY NUMBER: US 60/094, 190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 1743
 ; LENGTH: 1405
 ; TYPE: DNA
 ; ORGANISM: *Pseudomonas aeruginosa*
 ; US-09-252-991A-12452/C

Query Match 1.3%; Score 19; DB 4; Length 405;
 Best Local Similarity 100.0%; Pred. No. 18; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1040 CGCGCGCCCTGGCCCG 1058 ; Sequence 12452; Application US/09252991A
 Db 98 CGCGCGCCCTGGCCCG 80 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIORITY NUMBER: US 60/074, 788
 ; PRIORITY FILING DATE: 1998-02-18
 ; PRIORITY NUMBER: US 60/094, 190
 ; PRIORITY FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 1743
 ; LENGTH: 405
 ; TYPE: DNA
 ; ORGANISM: *Pseudomonas aeruginosa*
 ; US-09-252-991A-12452/C

PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 12452
 LENGTH: 414
 TYPE: DNA
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-12452

Query Match 1.3%; Score 19; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 821 CCAGTTCGACAACTGCCTG 839
 Db 255 CGAGTTCGACAACTGCCTG 237

RESULT 13

US-09-252-991A-8304

Sequence 8304, Application US/09252991A

PATENT NO. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196_136
 CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIORITY NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIORITY NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 8304

LENGTH: 489

TYPE: DNA

ORGANISM: *Pseudomonas aeruginosa*

Query Match 1.3%; Score 19; DB 4; Length 489;
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 821 CCAGTTCGACAACTGCCTG 839
 Db 423 CGAGTTCGACAACTGCCTG 441

RESULT 14

US-09-072-596-263

Sequence 263, Application US/09072596

PATENT NO. 6458366

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A. W.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Campos-Neto, Antonia
 APPLICANT: Houghton, Raymond
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Twardzik, Daniel R.
 APPLICANT: Lodes, Michael J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

NUMBER OF SEQUENCES: 350

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NUMBER OF SEQUENCES: 350

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/072,596
 FILING DATE: 05-MAY-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REFERENCE/DOCKET NUMBER: 31,392
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 622-6031
 INFORMATION FOR SEQ ID NO: 263:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 522 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-072-596-263

Query Match 1.3%; Score 19; DB 4; Length 522;
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1082 CGAGGCCAGCCTGGTGCCTG 1100
 Db 429 CGAGGCCAGCCTGGTGCCTG 447

Query Match 1.3%; Score 19; DB 4; Length 522;
 Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1082 CGAGGCCAGCCTGGTGCCTG 1100
 Db 429 CGAGGCCAGCCTGGTGCCTG 447

Query Match 1.3%; Score 19; DB 4; Length 723;
 Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 821 CCAGTTCGACAACTGCCTG 839
 Db 216 CCAGTTCGACAACTGCCTG 234

Search completed: August 14, 2003, 07:06:19
 Job time : 117 secs

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

RESULT 9
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
US-09-701-229-2 (1-448) x US-09-557-884-1 (1-1830121)
Qy 157 GluLeuTyrValLeuGluLeuSerSerPheGlnLeuGluThr 170
Db 1203588 GAACTTATGTACTAGAGCTTCTAGTTTCAGCTTGAGACA 1203629
RESULT 10
US-09-643-990A-1
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:

~~XXXXXX~~
polypeptide
with identity
to SEQID1
fragment
and comprises
> 25% of
SEQID1
+ encodes an
amino
acid
Sequence
of SEQID2.